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Box 18eg.
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I hereby Certify that this Correspondence is being deposited with the United States Postal Service as First Class Mail in an envelope addressed to: Assistant Commissioner for Patents, Washington, D.C. 20231 on January 18, 2002.

Corey Johnson

Name

Corey Johnson

Signature

January 18, 2002

Date of Signature

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Scott et al.

Serial No.: 09/873,881

Filed: June 4, 2001

For: Recombinant Multivalent Viral Vaccine

RESPONSE

Assistant Commissioner for Patents

Box Sequence

Washington, D.C. 20231

Sir:

In response to a Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, dated November 30, 2001, regarding sequence listing errors, Applicants herewith submit a corrected sequence listing as a Computer Readable Form and a Paper Copy. The CRF and the Paper Copy are the same. Applicants regret the error in the initial filing.

If any fee is due with this communication, please charge it to Deposit Account no. 08-2442.

Respectfully submitted,

HODGSON RUSS LLP

By

Ranjana Kadle
Ranjana Kadle Reg. No. 40,041

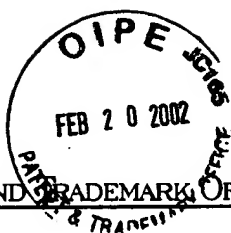
One M&T Plaza, Suite 2000
Buffalo, New York 14203-2391
(716) 848-1628

DATE: January 18, 2002

BFLODOCS: 648686 v1 (DWJ2011.DOC)



UNITED STATES PATENT AND TRADEMARK OFFICE



COMMISSIONER FOR PATENTS
UNITED STATES PATENT AND TRADEMARK OFFICE
WASHINGTON, D.C. 20231
www.uspto.gov

APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
09/873,881	06/04/2001	Fred W. Scott	18617.NEW

CONFIRMATION NO. 6373

FORMALITIES LETTER



OC00000007141372

Ranjana Kadle
Hodgson Russ LLP
Suite 2000
One M&T Plaza
Buffalo, NY 14203-2391

Date Mailed: 11/30/2001

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE
DISCLOSURES**

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

For questions regarding compliance to these requirements, please contact:

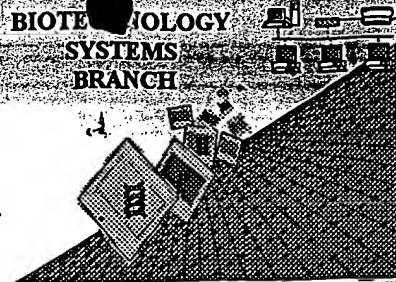
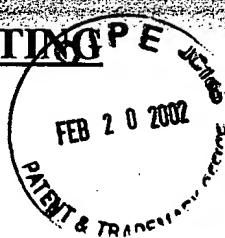
- For Rules Interpretation, call (703) 308-4216
- To Purchase PatentIn Software, call (703) 306-2600
- For PatentIn Software Program Help, call (703) 306-4119 or e-mail at patin21help@uspto.gov or patin3help@uspto.gov

*A copy of this notice **MUST** be returned with the reply.*

Customer Service Center
Initial Patent Examination Division (703) 308-1202

PART 2 - COPY TO BE RETURNED WITH RESPONSE

RAW SEQUENCE LISTING
ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/873,881A

Source: OIPK

Date Processed by STIC: 10/15/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/873,881A

DATE: 10/15/2001
TIME: 15:47:14

Input Set : A:\corrected sequence listing for Scott et al
Output Set: N:\CRF3\10152001\I873881A.raw

3 <110> APPLICANT: Scott, Fred W.
5 <120> TITLE OF INVENTION: Recombinant Multivalent Viral Vaccine
7 <130> FILE REFERENCE: 18617.0016
9 <140> CURRENT APPLICATION NUMBER: US 09/873,881A
10 <141> CURRENT FILING DATE: 2001-06-04
12 <150> PRIOR APPLICATION NUMBER: US 08/552,369
13 <151> PRIOR FILING DATE: 1995-11-03
15 <160> NUMBER OF SEQ ID NOS: 19

Does Not Comply
Corrected Diskette Needed

pg 1,3-4

ERRORED SEQUENCES

932 <210> SEQ ID NO: 19
933 <211> LENGTH: 1979
934 <212> TYPE: DNA
935 <213> ORGANISM: feline leukemia virus
937 <220> FEATURE:
938 <223> OTHER INFORMATION:
940 <400> SEQUENCE: 19
941 accaccaatc aagacctctc ggacagcccc agctcagacg atccatcaag 50
943 atg gaa agt cca acg cac cca aaa ccc tct aaa gat aag act ctc 95
944 Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu
945 1 5 10 15
947 tcg tgg aac tta gcg ttt ctg gtg ggg atc tta ttt aca ata gac 140
948 Ser Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp
949 20 25 30
951 ata gga atg gcc aat cct agt cca cac caa ata tat aat gta act 185
952 Ile Gly Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr
953 35 40 45
955 tgg gta ata acc aat gta caa act aac acc caa gct aac gcc acc 230
956 Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr
957 50 55 60
959 tct atg tta gga acc tta acc gat gcc tac cct acc cta cat gtt 275
960 Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val
961 65 70 75
963 gac tta tgt gac cta gtg gga gac acc tgg gaa cct ata gtc cta 320
964 Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Ile Val Leu
965 80 85 90
967 aac cca acc aat gta aaa cac ggg gca cgt tac tcc tcc tca aaa 365
968 Asn Pro Thr Asn Val Lys His Gly Ala Arg Tyr Ser Ser Ser Lys
W--> 969 95 100 105
971 tat gga tgt aaa act aca gat aga aaa aaa cag caa cag aca tac 410
972 Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr
973 110 115 120
975 ccc ttt tac gtc tgc ccc gga cat gcc ccc tcg ttg ggg cca aag 455
976 Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys
W--> 977 125 130 135

*numbers are
in bold print
due to error
above - apostrophe*

RAW SEQUENCE LISTING

DATE: 10/15/2001

PATENT APPLICATION: US/09/873,881A

TIME: 15:47:15

Input Set : A:\corrected sequence listing for Scott et al

Output Set: N:\CRF3\10152001\I873881A.raw

979 gga aca cat tgt gga ggg gca caa gat ggg ttt tgt gcc gca tgg 500
 980 Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp
 W--> 981 140 145 150
 983 gga tgt gag acc acc gga gaa gct tgg tgg aag ccc acc tcc tca 545
 984 Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser
 W--> 985 155 160 165
 987 tgg gac tat atc aca gta aaa aga ggg agt agt cag gac aat agc 590
 988 Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser
 W--> 989 170 175 180
 991 tgt gag gga aaa tgc aac ccc ctg gtt ttg cag ttc acc cag aag 635
 992 Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys
 W--> 993 185 190 195
 995 gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga 680
 996 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg
 W--> 997 200 205 210
 999 cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc 725
 1000 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser
 W--> 1001 215 220 225
 1003 cgg cag gta tca acc att acg ccg cct cag gca atg gga cca aac 770
 1004 Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn
 W--> 1005 230 235 240
 1007 cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca 815
 1008 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr
 W--> 1009 245 250 255
 1011 ggg tcc aaa gtg gcg acc cag agg ccc caa acg aat gaa agc gcc 860
 1012 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala
 W--> 1013 260 265 270
 1015 cca agg tct gtt gcc ccc acc acc atg ggt ccc aaa cgg att ggg 905
 1016 Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly
 W--> 1017 275 280 285
 1019 acc gga gat agg tta ata aat tta gta caa ggg aca tac cta gcc 950
 1020 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala
 W--> 1021 290 295 300
 1023 tta aat gcc acc gac ccc aac aaa act aaa gac tgt tgg ctc tgc 995
 1024 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys
 W--> 1025 305 310 315
 1027 ctg gtt tct cga cca ccc tat tac gaa ggg att gca atc tta ggt 1040
 1028 Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly
 W--> 1029 320 325 330
 1031 acc tac agc aac caa aca aac ccc ccc cca tcc tgc cta tct act 1085
 1032 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile
 W--> 1033 335 340 345
 1035 ccg caa cac aaa cta act ata tct gaa gta tca ggg caa gga atg 1130
 1036 Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met
 W--> 1037 350 355 360
 1039 tgc ata ggg act gtt cct aaa acc cac cag gct ttg tgc aat aag 1175
 1040 Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys
 W--> 1041 365 370 375
 1043 aca caa cag gga cat aca ggg gcg cac tat cta gcc gcc ccc aac 1220

RAW SEQUENCE LISTING

DATE: 10/15/2001

PATENT APPLICATION: US/09/873,881A

TIME: 15:47:15

Input Set : A:\corrected sequence listing for Scott et al

Output Set: N:\CRF3\10152001\I873881A.raw

1044 Thr Gln Gln Gly His Thr Gly Ala His Tyr Leu Ala Ala Pro Asn
 W--> 1045 380 385 390
 1047 ggc acc tat tgg gcc tgt aac act gga ctc acc cca tgc att tcc 1265
 1048 Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu Thr Pro Cys Ile Ser
 W--> 1049 395 400 405
 1051 atg gcg gtg ctc aat tgg acc tct gat ttt tgt gtc tta atc gaa 1310
 1052 Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys Val Leu Ile Glu
 W--> 1053 410 415 420
 1055 tta tgg ccc aga gtg act tac cat caa ccc gaa tat gtg tac aca 1355
 1056 Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr Val Tyr Thr
 W--> 1057 425 430 435
 1059 cat ttt gcc aaa gct gtc agg ttc cga aga gaa cca ata tca cta 1400
 1060 His Phe Ala Lys Ala Val Arg Phe Arg Arg Glu Pro Ile Ser Leu
 W--> 1061 440 445 450
 1063 acg gtt gcc ctt atg ttg gga gga ctt act gta ggg ggc ata gcc 1445
 1064 Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile Ala
 W--> 1065 455 460 465
 1067 gcg ggg gtc gga aca ggg act aaa gcc ctc ctt gaa aca gcc cag 1490
 1068 Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln
 W--> 1069 470 475 480
 1071 ttc aga caa cta caa atg gcc atg cac aca gac atc cag gcc cta 1535
 1072 Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu
 W--> 1073 485 490 495
 1075 gaa gaa tca att agt gcc tta gaa aag tcc ctg acc tcc ctt tct 1580
 1076 Glu Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser
 W--> 1077 500 505 510
 1079 gaa gta gtc tta caa aac aga cgg ggc cta gat att cta ttc tta 1625
 1080 Glu Val Val Leu Gln Asn Arg Arg Glu Leu Asp Ile Leu Phe Leu
 W--> 1081 515 520 525
 1083 caa gag gga ggg ctc tgt gcc gca ttg aaa gaa gaa tgt tgc ttc 1670
 1084 Gln Glu Gly Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe
 W--> 1085 530 535 540
 1087 tat gcg gat cac acc gga ctc gtc cga gac aat atg gcc aaa tta 1715
 1088 Tyr Ala Asp His Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu
 W--> 1089 545 550 555
 1091 aga gaa aga cta aaa cag cgg caa caa ctg ttt gac tcc caa cag 1760
 1092 Arg Glu Arg Leu Lys Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln
 W--> 1093 560 565 570
 1095 gga tgg ttt gaa gga tgg ttc aac aag tcc ccc tgg ttt aca acc 1805
 1096 Gly Trp Phe Glu Gly Trp Phe Asn Lys Ser Pro Trp Phe Thr Thr
 W--> 1097 575 580 585
 1099 cta att tcc tcc att atg ggc ccc tta cta atc cta ctc cta att 1850
 1100 Leu Ile Ser Ser Ile Met Gly Pro Leu Leu Ile Leu Leu Ile
 W--> 1101 590 595 600
 1103 ctc ctc ttc ggc cca tgc atc ctt aac cga tta gta caa ttc gta 1895
 1104 Leu Leu Phe Gly Pro Cys Ile Leu Asn Arg Leu Val Gln Phe Val
 W--> 1105 605 610 615
 1107 aaa gac aga ata tct gtg gta cag gct tta att tta acc caa cag 1940
 W--> 1108 Lys Asp Arg Ile Ser Val Val Gln Ala Leu Ile Leu Thr Gln Gln

Initial
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RAW SEQUENCE LISTING

DATE: 10/15/2001

PATENT APPLICATION: US/09/873,881A

TIME: 15:47:15

Input Set : A:\corrected sequence listing for Scott et al

Output Set: N:\CRF3\10152001\I873881A.raw

W--> 1109 620 625 630
1111 tac caa cag ata aag caa tac gat ccg gac cga cca tga 1979
1112 Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp Arg Pro
W--> 1113 635 640
E--> 1117 bFLOdOcs:589477_1 (cm%d01)

Delete

589477

VERIFICATION SUMMARY

DATE: 10/15/2001

PATENT APPLICATION: US/09/873,881A

TIME: 15:47:16

Input Set : A:\corrected sequence listing for Scott et al

Output Set: N:\CRF3\10152001\I873881A.raw

L:21 M:283 W: Missing Blank Line separator, <220> field identifier
L:912 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:969 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:973 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:977 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:981 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:985 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:989 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:993 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:997 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1001 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1005 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1009 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1013 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1017 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1021 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1025 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1029 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1033 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1037 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1041 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1045 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
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L:1053 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1057 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1061 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1065 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1069 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1073 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1077 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1081 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1085 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1089 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1093 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1097 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1108 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:1109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1117 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1995 SEQ:19
L:1117 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:18
L:1117 M:112 C: (48) String data converted to lower case,
L:1117 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1979 Found:1995 SEQ:19